

## SEQUENCE LISTING

<110> Andrade-Gordon, Patricia

Darrow, Andrew

Qi, Jenson

<120> DNA encoding the human serine protease T

<130> ORT-1032

<140>

<141>

<160> 9

<170> PatentIn Ver. 2.0

<210> 1

<211> 1110

<212> DNA

<213> Homo sapiens

<400> 1

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ccaggatgct gaac cgaatg gtggg cgggc aggaca cgca ggagggc gag tggccctggc 180

aagt cagcat ccag cgca ac ggaagg ccact tctgcg gggg cagcctcatc gggagca gt 240

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agg tggagag caac cccctg tacca gggca cggcct ccag cgctgac gtg gccc tgggtgg 420

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1020  
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1110

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 2

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20

<210> 3

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 3

tgcgtggat gctgacttgc

20

<210> 4

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nested probe

<400> 4

ccagaggatgct gaac cgaatg gtgggcgggc aggaca cgca

40

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 5

aggatctaga ggaggcgcgag tggccctggc

30

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 6

ggggtctaga cttctggccg cccaaacctcg

30

<210> 7

<211> 290

<212> PRT

<213> Homo sapiens

<400> 7

Met Arg Arg Pro Ala Ala Val Pro Leu Leu Leu Leu Cys Phe Gly

1

5

10

15

Ser Gln Arg Ala Lys Ala Ala Thr Ala Cys Gly Arg Pro Arg Met Leu

20

25

30

Asn Arg Met Val Gly Gly Gln Asp Thr Gln Glu Gly Glu Trp Pro Trp

35

40

45

Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser Leu

50

55

60

Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn Thr

65

70

75

80

Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu Val

85

90

95

Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu Ser

100

105

110

Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu Val

115

120

125

Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val Cys

130

135

140

Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp Val

145

150

155

160

Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro Arg

165

170

175

Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys Asn

180

185

190

Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr Ile

195

200

205

Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp Ala

210

215

220

Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln Ser

225

230

235

240

Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg Gln

245

250

255

Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp Ile

260

265

270

His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly Gly

275

280

285

Gln Lys

290

<210> 8

<211> 1130

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Fusion gene of

Protease T in a zymogen activation vector

&lt;400&gt; 8

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gtggacgcgg ccgcctttgc tgccccctt gatgatgatg acaagatcgt tggggctat 180  
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1020  
agtttggaca aacc acaact agaat gcagt gaaaaaaatg ctttatttgt gaaatttg tg  
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1130

<210> 9

<211> 315

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein

of Protease T in a zymogen activation construct

<400> 9

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1 5 10 15

Val Val Ser Asn Leu Leu Leu Cys Gln Gly Val Val Ser Asp Tyr Lys

20

25

30

Asp Asp Asp Asp Val Asp Ala Ala Ala Leu Ala Ala Pro Phe Asp Asp

35

40

45

Asp Asp Lys Ile Val Gly Gly Tyr Ala Leu Glu Glu Gly Glu Trp Pro

50

55

60

Trp Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser

65

70

75

80

Leu Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn

85

90

95

Thr Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu

100

105

110

Val Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu

115

120

125

Ser Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu

130

135

140

Val Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val

145

150

155

160

Cys Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp

165

170

175

Val Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro

180

185

190

Arg Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys

195

200

205

Asn Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr

210

215

220

Ile Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp

225

230

235

240

Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln

245

250

255

Ser Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg

260

265

270

Gln Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp

275

280

285

Ile His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly

290

295

300

Gly Gln Lys Ser Arg His His His His His

305

310

315